

REPLACEMENT SHEET

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The intron sequences between exons 2 - 3 and exons 18 - 19 are missing (introns: small letters, exons: capital letters). Small letters in the first exon indicate nucleotides that have not been unambiguously determined.

Exon 1

```
1  CGGGTGAATC CCGGCGCCGC GCCCGGACC CGCAGCTCCC TGCACCTCTC
51  CCTCCCAGCC GCTTTAACAC CCACACCCCA CAGTCTCTCC CACGsCCGCG
101 CCTTGGCGGC CCCACTGAAT CCCTACGCGG GGCCAGCGG TACCGGGAGA
151 CCGGGCTAGC CTATGGGAGC GCCCAGATAA CGCGGGTTGG GGGCGCCCGC
201 GCCCCcATCC CCGCCAGCAT GACTCGATCG CCGCCCCCTCA GAGAGCTGCC
251 CCCGAGTTAC ACACCCCCAG CTCGAACCGC AGCACCCCAG gtgagtagag
301 ggggagctgg aagaaggaag agagcggagc caggtctgtc actcgggcct
351 ctgcaagggtt tgtgatgtct tgaagtgccg agtgtcatta gatgtctgaa
401 ggcaagttag agccagcacc gcaagcaagt tgtgcgtgtg tgtcgggtgtg
451 tctgtgccgg tgtctcctca tcgtctggcc agtgagaatg aatgtctgtg
501 ggttcacctc tgtgtccacc cgacgacagg tgtgtgtaca tatgtatcct
551 gctctcagaa aatgggccta tgccgccggg cgcggtgact cacgcctgta
601 atcccaacac tgggaggctg aggcaggcag attacctgag gtcaggaggtt
651 cgagaccagc caggccaaca tggggaaact ctgtctctac taaaaataaa
701 aattagcagg gcgtggtggc gggcgccctgt agtcccaact actcgggagg
751 ctgaggcagg agaatctctt gaacctggga ggcggaggtt gcagtcaagc
801 cgagatcaca cactgcact ccagccaggg caacagagcg agatgcgtct
851 caaaaaaaaa aaaaaaaaaa aaaaggagag aaaacaaaaa gaaaagaaag
901 gaaaataggc ctatgccttc ctcagggtgtg tgctggggat ggtgggtggt
951 acatcttcca agtctgggcc tgtgtctgtg ttggtgctcc ctgtcccaca
1001 tccagaaatc aagaagcgag ggctgggcag cagatatata gggtgagaag
```

Fig.1A

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1051 ggaaggattt catgcattgt tacagtgatg cctggctgac ctttctcttt
      EXON 2
1101 ccatccccagA TCCTAGCTGG GAGCCTGAAG GCTCCACTCT GGCTTCGTGC
1151 TTA CTTCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT
1201 GTGGCAAAGT GCTCTTTCTG GGACTGTTGG CCTTTGGGGC CCTGGCATT
1251 GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA
1301 AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA TTACACCAAG GAGAAGCTGG
1351 GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG
1401 GAGGGAGAGA ACATCCTCAC ACCCGAAGCA CTTGGCCTCC ACCTCCAGGC
1451 AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAG.....
1501 .....g
1551 tgagtctggc tgagcccctg agcagctggg ggcgaggcgt gctgtggggg
1601 ttctggagtg ggaatcccct tcttctgctg atctcctatg cccctggcta
      EXON 4
1651 ttgcagTCCT GGGATTTGAA CAAAATCTGC TACAAGTCAG GAGTTCCCCCT
1701 TATTGAAAAT GGAATGATTG AGCGGgtaag tgtcctgaga gggagtagag
1751 gcagaacttt ttctgtagcg tgggaggact cagagaccga gcaagcccca
1801 cagcctgcaa tctgccccct taaaactaag gagggggatt gcagagggga
1851 tcctacaaag gttgtggggc aggactgacg tggcccgggg tatccctggc
      EXON 5
1901 agATGATTGA GAAGCTGTTT CCGTGCGTGA TCCTCACCCC CCTCGACTGC
1951 TTCTGGGAGG GAGCCAAACT CCAAGGGGGC TCCGCCTACC TGCCgtgagt
2001 gccactcctg gggccctgct tcattctccc ctggggactc tcccagcaga
2051 aaggaggggt ctggggaatg aggatgatca aaaccttacc aaggtcctaa
2101 ttacctcca ggccaggaac agagagcatg ggcttcccca aggtctctct
2151 cacatcctcc ttctctttcc ctctcaagga aggaagacct gacttattta
2201 cacaaaacta aacacaaaga tctgtaagat ctgagcaaag gagaaaaaga
2251 tccccacaaa gaggttttgc tgggggaaat tacctaggtg tttgctaagc
2301 cattgcccag gccagaaaga aaacctgcta caggcatgtg cctgctggtt
2351 gtatattaga accaagcaca cagcttggtg aggaactcag tggggccttt

```

Fig.1B

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2401 ctgggcccctt tctatgtatt aggtaaccct gccctgatat tcgtctcagc
 2451 cccttggtact cttctacagc tctactgtage accctgggtg gcccatgcag
 2501 cctggcagtt ctgagaagct gaggcttgca caccctccat atggaaggac
 2551 aaatcggcag ataagaggag ggtgggggtac agcatggcgc cccagcagca
 2601 gtttggagcc tgggttttcg tccctgaccc tcaccaacta taggcttttc
 2651 cctcagCGGC *EXON 6* CGCCCGGATA TCCAGTGGAC CAACCTGGAT CCAGAGCAGC
 2701 TGCTGGAGGA GCTGGGTCCC TTTGCCTCCC TTGAGGGCTT CCGGGAGCTG
 2751 CTAGACAAGG CACAGGTGGG CCAGGCCTAC GTGGGGCGGC CCTGTCTGCA
 2801 CCCTGATGAC CTCCACTGCC CACCTAGTGC CCCCACCAT CACAGCAGGC
 2851 AGgtgggttc caaccaggtc tgccaggga aggtgtttt cttcccttt
 2901 cccttcctca tactcctgtg ttctggggga gctgactgct ctgtgcctg
 2951 accccccact tcctggccat tattaccctg ctcccacagt gccaggcccc
 3001 caatgttcca ttccattca gttatcctac ggagccctca agtggatat
 3051 atgaatccct ttttccttt ctaagcctag ataaggctg acttctttt
 3101 ttttttttt ttgagtctca ctctgtcacc caggctggag tgcagtagtt
 3151 cgatcttggc tctctgcaac ctctggtcaa gcaattctcc tgccttagcc
 3201 tcctgagtag ctgggattac aggtgcccac caccatgcc ggctaatttt
 3251 tattagcctc ccaaagtgt gggattacag gcgtgagcca ctgcgcctgg
 3301 ccaaggctgg actttttatc aaaatagact aatacaggga aactaagaac
 3351 acagcaggta agcatgaata tcatacctgg tttcccaggt ttctttgtgg
 3401 ccctgcaa at gtggtacttt tttcagaatc cgccagttac accagtcct
 3451 cccagaagcc tacttccagg cctctgcttc cccttggggc ttctgtctg
 3501 cgggatacta gctgttctact cctgcagagc agtcaagagg ctgagaatag
 3551 ttacctacac tccagcccta ctgagcttca tggcagcgtg gttcctggag
 3601 gtggaagccc agggacactc agttatccac ggccagggcc ttgagcatta
 3651 acccctcctg tttccctcca *EXON 7* gGGCTCCCAA TGTGGCTCAC GAGCTGAGTG
 3701 GGGGCTGCCA TGGCTTCTCC CACAAATTCA TGCACTGGCA GGAGGAATTG

Fig.1C

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3751 CTGCTGGGAG GCATGGCCAG AGACCCCCAA GGAGAGCTGC TGAGGtaggg
 3801 tctcctctgg gagttggtga ggggactctg ttcattgagaa cccatactgt
 3851 aatgccaggc agctctggca aaaggccctt cacatccctc accaggtggt
 3901 tggggcagct ctgacccttg gttctccac acccccacca gGGCAGAGGC
 3951 CCTGCAGAGC ACCTTCTTGC TGATGAGTCC CCGCCAGCTG TACGAGCATT
 4001 TCCGGGGTGA CTATCAGACA CATGACATTG GCTGGAGTGA GGAGCAGGCC
 4051 AGCACAGTGC TACAAGCCTG GCAGCGGCGC TTTGTGCAGg tcggtatgga
 4101 caaggacaag gggggtgccc tgaggccatt cctcctcct gccccctcct
 4151 atccaccctg tttctccagC TGGCCAGGA GGCCCTGCCT GAGAACGCTT
 4201 CCCAGCAGAT CCATGCCTTC TCCTCCACCA CCCTGGATGA CATCCTGCAT
 4251 GCGTTCTCTG AAGTCAGTGC TGCCCGTGTG GTGGGAGGCT ATCTGCTCAT
 4301 Ggtgggtctt gcacctggca ccttgcccc accccacctc caaccagtgc
 4351 ccaccctggg agcccttgag actgcccctt cccccacag CTGGCCTATG
 4401 CCTGTGTGAC CATGCTGCGG TGGGACTGCG CCCAGTCCCA GGGTTCCGTG
 4451 GGCCTTGCCG GGGTACTGCT GGTGGCCCTG GCGGTGGCCT CAGGCCTTGG
 4501 GCTCTGTGCC CTGCTCGGCA TCACCTCAA TGCTGCCACT ACCCAGgtac
 4551 gccaggactg cagggcagac tcagtgccag tcaccaggct tcacgggtcc
 4601 tcagctgccc gctcctctgc cctccagGT GCTGCCCTTC TTGGCTCTGG
 4651 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCCTT CACAGAGGCT
 4701 CTGCCTGGCA CCCCTCTCCA Ggtggggcct tgtccccag ggctcatctg
 4751 aggcagctca gcttactggt taagagcctc ttggttcaag tgacccttgg
 4801 gctgctaatag aacctcggtg cctcttgtcc ccatctgtaa acaggggaaa
 4851 taatagtgtc gtgtcctaag gggtattggt tggatcagtg aggttaactca
 4901 agttgaatgc ttagaacagc ccatcatagc tacatggtac ccaataaatg
 4951 ctagccactg tggtatgact gccccacctc tgcaccccaa gttcctgagc
 5001 ccccccttca ctccactttg acacggcccc tcccttgtga cctgagggca
 5051 ggtccccact ctgtcctggc agGAGCGCAT GGGCGAGTGT CTGCAGCGCA

Fig.1D

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5101 CGGGCACCAG TGTCGTACTC ACATCCATCA ACAACATGGC CGCCTTCCTC
 5151 ATGGCTGCCC TCGTTCCCAT CCCTGCGCTG CGAGCCTTCT CCCTACAGGC
 5201 GGCCATAGTG GTTGGCTGCA CCTTTGTAGC CGTGATGCTT GTCTTCCCAG
 5251 CCATCCTCAG CCTGGACCTA CGGCGGCGCC ACTGCCAGCG CCTTGATGTG
 5301 CTCTGCTGCT TCTCCAGgta ctgcggtgcgc cccagccccct tcctccccgtg
 5351 acccagccca gcctgtcccc tcaccagcat ttcaaggcac agacctgtca
 5401 tccactctct acctcttcca gTCCCTGCTC TGCTCAGGTG ATTCAGATCC
 EXON 13
 5451 TGCCCCAGGA GCTGGGGGAC GGGACAGTAC CAGTGGGCAT TGCCCACCTC
 5501 ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT
 5551 GGTCACCATC CTGCCTCCCC AAGCCACCT GGTGCCCCCA CCTTCTGACC
 5601 CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GGTCCACACG GGACCTTCTA
 5651 GGCCAGGAGG AGGAGACAAG GCAGAAGGCA GCCTGCAAGT CCCTGCCCTG
 5701 TGCCCGCTGG AATCTTGCCC ATTTGCGCCG CTATCAGTTT GCCCCGTTCG
 5751 TGCTCCAGTC ACATGCTAAG gtaagactgg gcagagcagg gcagagactt
 5801 agcatctctg ggcccagaag ggcagagagg gcttagtcca ctgcctgagg
 5851 ggctgggggc agccctgggg tctccagctt agttgctaca tcccgcagGC
 EX
 XON 14
 5901 CATCGTGCTG GTGCTCTTTG GTGCTCTTCT GGGCCTGAGC CTCTACGGAG
 5951 CCACCTTGGT GCAAGACGGC CTGGCCCTGA CGGATGTGGT GCCTCGGGGC
 6001 ACCAAGGAGC ATGCCTTCCT GAGCGCCCAG CTCAGGTACT TCTCCCTGTA
 6051 CGAGGTGGCC CTGGTGACCC AGGGTGGCTT TGA CTACGCC CACTCCCAAC
 6101 GCGCCCTCTT TGATCTGCAC CAGCGCTTCA GTTCCCTCAA GGCGGTGCTG
 6151 CCCCCACCGG CCACCCAGGC ACCCCGCACC TGGCTGCACT ATTACCGCAA
 6201 CTGGCTACAG Ggtgagaggc gaggagacgg gcagggaggg gtgctgcagg
 6251 gagaaacgcc ctggggccac cagctaataa aaccctatcc tgggtctcccc
 EXON 15
 6301 cagGAATCCA GGCTGCCTTT GACCAGGACT GGGCTTCTGG GCGCATCACC
 6351 CGCCACTCGA CCGCAATGGC TCTGAGGATG GGGCCCTGGC CTACAAGCTG
 6401 CTCATCCAGA CTGGAGACGC CCAGGAGCTT CTGGATTTCa GCCAGgttgg

Fig.1E

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6451 gagagggctg gaggggtcca ctagtacagg ggctgcaggc ctcctgggcc
EXON 16
6501 caggccttca gccctctctg cctctgcagC TGACCACAAG GAAGCTGGTG
6551 GACAGAGAGG GACTGATTCC ACCCGAGCTC TTCTACATGG GGCTGACCGT
6601 GTGGGTGAGC AGTGACCCCC TGGGTCTGGC AGCCTCACAG GCCAACTTCT
6651 ACCCCCCACC TCCTGAATGG CTGCACGACA AATACGACAC CACGGGGGAG
6701 AACTTTCGCA gtgagtcttg gggggagctc ggcaagagcc tcagcctcgc
6751 ccacacaagc cctgagcctg aggccctgcc cactctgccc cgtgctcacc
EXON 17
6801 gccctgtccc tctccctctt ctcccttccc ctccccctcca cagTCCCGCC
6851 AGCTCAGCCC TTGGAGTTTG CCCAGTTCCC TTTCTGCTG CGTGGCCTCC
6901 AGAAGACTGC AGACTTTGTG GAGGCCATCG AGGGGGCCCCG GGCAGCATGC
6951 GCAGAGGCCG GCCAGGCTGG GGTGCACGCC TACCCCAGCG GCTCCCCCTT
7001 CCTCTTCTGG GAACAGTATC TGGGCCTGCG GCGCTGCTTC CTGCTGGCCG
7051 TCTGCATCCT GCTGGTGTGC ACTTTCCTCG TCTGTGCTCT GCTGCTCCTC
7101 AACCCTTGA CGGCTGGCCT CATAgtagt gcttgcagga gtggggacag
7151 agacacccca cccttccctg cccagcctgt catccctcct gccaggagcc
EXON 18
7201 ctctgtgagc cctgtctccc tcagGTGCTG GTCCTGGCGA TGATGACAGT
7251 GGAACCTCTT GGTATCATGG GTTTCCTGGG CATCAAGCTG AGTGCCATCC
7301 CCGTGGTGAT CCTTGTGGCC TCTGTAGGCA TTGGCGTTGA GTTCACAGTC
7351 CACGTGGCTC TGGGCTTCCT GACCACCCAG GGCAGCCGGA ACCTGCGGGC
7401 CGCCCATGCC CTTGAGCACA CATTTGCCCC CGTGACCGAT GGGGCCATCT
7451 CCACATTGCT GGGTCTGCTC ATGCTTGCTG GTTCCCATT TGACTTCATT
7501 GTAAG.....
7551 gtagggaggg ctcggggcag ggaggcaggg ctcaggacag
EXON 20
7601 gcctgggctg actccccca caccctaccc ctagGTACTT CTTTGC GGCG
7651 CTGACAGTGC TCACGCTCCT GGGCCTCCTC CATGGACTCG TGCTGCTGCC
7701 TGTGCTGCTG TCCATCCTGG GCCCGCCGCC AGAGgtgacc acaccctcgg
7751 caccatccct ctactcccag cccaagggac ggggtaggga gaggcaaggg

Fig.1F

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7801 aagggacaga gccctgtggc ccacagacag gtacctcccc aacaggtgcc
7851 accagctgaa ggtggcagcc tcctcctttc cccagacacc atgttcctgc
7901 ccctcagccc tcctggcttc ttcattgggac ccaccttaga ctttttaggat
7951 ccagaacaag gtgcagggtt tgccccaggc ctcaacatcc tgtgcctgc
8001 cagctctcat atcctgctgg agaccaacaa gggccccagc ttcccaacag
8051 tcatggtaat cccagcgag atgctaaagg ggacgggagc cccaggggcc
8101 cgtgggctta ctggggctgg tgtctcccca ^{EXON 21} cagGTGATAC AGATGTACAA
8151 GGAAAGCCCA GAGATCCTGA GTCCACCAGC TCCACAGGGA GCGGGCTTA
8201 Ggtggggggc atcctcctcc ctgccccaga gctttgccag agtgactacc
8251 tccatgaccg tggccatcca cccaccccc ctgcctggtg cctacatcca
8301 tccagcccct gatgagcccc cttggctccc tgctgtcact agctctggca
8351 acctcagttc caggggacca ggtccagcca ctgggtgaaa gagcagctga
8401 agcacagaga ccatgtgtgg ggcgtgtggg gtcactggga agcactgggt
8451 ctggtgttag acgcaggatg gaccctgga gggctctgct gctgctgcat
8501 cccctctccc gaccagctg tcatgggcct ccctgatatc catacagaac
8551 agccaccgat ttgcacatcc aggctgtgt gagcctgtat ctgtgtcact
8601 tgagagtga agctggcact tggggctgca gtgcagccct gtcctcttc
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8701 gcaccttcc gtctggtgac tcctgggcag gctctccata tcctgcca
8751 cctcctacca catccattat ttatatgaaa atgtctatct tttgagtata
8801 catacatgtt agctatgatg aaagttttat tttttaaaga atgaaatata
8851 ttctatgtga agctatgatg aaagttttat tttttaaaga atgaaatata
8901 ttctatgtga actaatctcg aaagttttat tttttaaaga atgaaatata
8951 ttctatgtgt gcaagtgaac attagcttca gttgcttttt tttggacaga
9001 gtggggagtt tgcaagtga ccttagctat tggaaggagc ttctctggtg
9051 ccaggacctg aggtattagc ttctctagtt ctgggtggaa aagacccag
9101 attctggatt tttgtcatat acttggtaac atcatctgga ttaagtgtt

Fig.1G

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```

9151 actatacaaa acgataacaa attttgttgg tgtgaaatcc tactggggtc
9201 aatctggaga ccgagagcag aaaaaaaaga accccactgt gtggctttca
9251 gagccaccat attccagcct gcccgtctct ccagactcac ctccacctac
9301 ctgcttcacc cgcacgggaa acggcaaggc agaggggcaa agccatgcag
9351 caggtggaag gcgaggtgga ggcagatcag gaaagcagcc agttgaagca
9401 gagagaggtc aacagggctt ggggagcttc tcaggaggtt tgtggacca
9451 gggaaaggag ccaggttcca gagcaacctc caaggcaaag gcctctgtaa
9501 gttggttgtc ctgacagccg agaggtgtct ttggccagtc agccagtgga
9551 tcagttgctg gaactgctca gaaactgagg tgctagcagt tagtgaggac
9601 acagcgtaag ttgtttgttc tgtgaaagtt gaacagctcc actaagcaga
9651 ggccttgaag agtggccaca gccctggaat agagcacaga gcctcaccta
9701 gaggcgtggg gaggtttgca actgcccctt cccagccata gcttaggacc
9751 catagtctag ttcacataga ccctgggctc caaccacca ctcaccagga
9801 atgatccac cccaggaaca atgcgttctc acatcccacc ccacctggac
9851 aaaggccagg aaatcatggt ctgacaaaaa gatacaacaa caaaaacaac
9901 aacaacaaaa aacgcctatt gcaattgaat ccacgctaaa atgcctaaaa
9951 agctcaagag aagcgggtag ttggcagaga acctagagta gggggtgcaa
10001 ccagcaggcc caagggaggg aggetgcatt tgggtccagc agtgtttggg
10051 tcaccaagaa gggccttcta ggtggagcag agagagctca ccaggccaga
10101 atagtgcaa gggggtcagc cctcagtgcc acttaccagc ggagtaaccc
10151 tgggcaagtt agccagcctc actaagcctc cccatcttca tctttccagG
      XON 22
10201 CCCGAGGAGA TCTAGCCTCT GCCTCCCACC CCAGCACCCC CTCATCAGAC
10251 ACAAGGAGCG CCACTGTCTG GACAGGCTGA ATTGGTCTTC GGGTCCCTAA
10301 TTTCTCATAC GCCATTCCCT CTGCCTAGAA CACTTTCTCA CCTCCCCTTG
10351 ATGTGACCCC ATATCACCTT TCGAGGTGAA TTGGATCGGA TGCCATCTCC
10401 TCCAGGAGGG GTGGGGTCGT GCCTCCTGTG AGGTCCCAGT GCCCCTGAGT
10451 GTCTGTGCCC GTCTGTTTCC CCGTCCCTCT CTCTAAGCCC GGAGGCTTAC

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Fig.1H

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10501 TGCGGGTAAG GACGGCGGGA CAGGACCTTA ACCCCTGGGA CGAACACCAG
10551 CTCCGCAAAG GACTCCGCAC CCGGCGCCGC CCACGGGGTG CGGGTCCCAG
10601 GAGGACCAGC AGAGAGGAGC ATAGGAGAGC AAAGGAGATC AGTGACCCAT
10651 GGCTTCCCCG GTGGCGCGGA ACAGCCCGGA GCCGCCTGTG ATTTGCATAC
10701 CCATGGTGCA CCACGAAAAG ATACCCTCAA GATGCTTGCA CTCCCTCTGT
10751 GCGCGCATTT CTGCACTGTT TTAGAGCATG ATGCCTCTTA CACGCATCTG
10801 TGTGCATAAA CTACATATAG GGAGTGCGTA CCACGCAGGC ATCCAACAAC
10851 CATAAGTGTG TTAAGTGTTA GTTCTCCCTG CGAGGTTCGA AGCGGAAGTC
10901 ACGAATATAC TCGGGTTTCT CTTCAAAGCG CATAAATCTT TCGCCTTTTA
10951 CTAAAGATTT CCGTGGAGAG AAAGTTGTGA GTTTTATTC AATTTTTTGA
11001 GGCCTCTTAT TTCCTGAGGC TACATTTTTA AGTATTAAAA GTTAGGCAAC
11051 TACAAAAAAA AAAAAAAA

Fig.1I

REPLACEMENT SHEET

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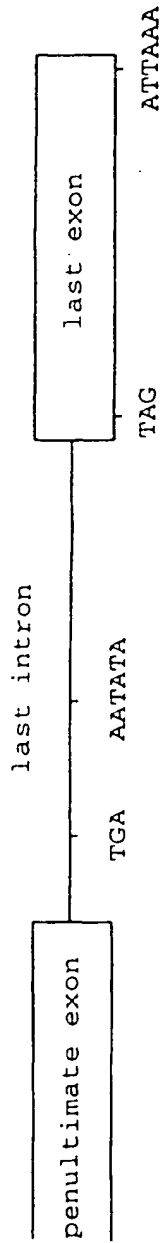
1 .....MTRSPPLRELP..... 11
  |...|
1 MASAGNAAE PQDRGGGSGCIGAPGRPAGGGRRRRTGGLRRAAAPDRDYL 50
12 ..PSYTPPARTAAPQI...LAGSLKAPLWLRAYFQGLLFSLGCGIQRHCG 56
  |||...| |...| |...| |...| |...| |...| |...|
51 HRPSYCDAA.FALEQISKGKATGRKAPLWLRKFQRLLFKLGCYIQKNCG 99
57 KVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGE 106
  |...| |...| |...| |...| |...| |...| |...| |...|
100 KFLVVGLLIFGAFVGLKAANLETNVEELWVEVGGRVSRELNTRYQKIGE 149
107 EAAYTSQMLIQATARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDL 156
  ||...| |...| |...| |...| |...| |...| |...| |...|
150 EAMFNPQLMIQTPKEEGANVLTTEALLQHLDLSALQASRVHVYMYNRQWKL 199
157 NKICYKSGVPLIENGMIERMIEKLFPCVILTPLDCEWEGAKLQGG SAYLP 206
  :...| |...| |...| |...| |...| |...| |...| |...|
200 EHLCKYSGELITETGYMDQII EYLYPCLII TPLDCFWEGAKLQSGTAYLL 249
207 GRPDIQWTNLDPEQLLEELGPFA.SLEGFRELLDKAQVGQAYVGRPCLHP 255
  |...| |...| |...| |...| |...| |...| |...| |...|
250 GKPLRWTFNFDPLEFLEELKKINYQVDSWEMLNKAEVGHGYMDRPNLP 299
256 DDLHCPPSAPNHHSRQAPNVAHELSSGCHGFSHKFMHWQEELLGGMARD 305
  .|...| |...| |...| |...| |...| |...| |...| |...|
300 ADPDCPATAPNKNSTKPLDMALVLNCGCHGLSRKYMHWQEELIVGGTVKN 349
306 PQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAW 355
  .|...| |...| |...| |...| |...| |...| |...| |...|
350 STGKLVSAAHALQTMFQLMTPKQMYEHFKGYEYVSHINWNEDKAAAIL EAW 399
356 QRRFVQLAQEALPENASQQIHAFSSTLDDILHAFSEVSAARVVGGYLLM 405
  ||...| |...| |...| |...| |...| |...| |...| |...|
400 QRTYVEVVHQSV AQNSTQKVLSTTTTLLDDILKSFSDVSVIRVASGYLLM 449
406 LAYACVTMLRWDCAQSGSVGLAGVLLVALAVASGLGLCALLGITFNAAT 455
  ||||...| |...| |...| |...| |...| |...| |...| |...|
450 LAYACLTMLRWDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAAT 499
456 TQVLPFLALGIGVDDVFLLAHAFTEALPG..TPLQERMGECLQRTGTSVV 503
  ||||...| |...| |...| |...| |...| |...| |...| |...|
500 TQVLPFLALGVGVDDVFLLAHAFSETGQNKRI PFEDRTGECLKRTGASVA 549
504 LTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLD 553
  ||||...| |...| |...| |...| |...| |...| |...| |...|
550 LTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLLIFPAILSMD 599
554 LRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGT.....VPVG 592
  |...| |...| |...| |...| |...| |...| |...| |...|
600 LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHS 649
593 IAH.....LTATVQAFTHCEASSQHVVITLPPQAHL...VPPPSDPLGS 633
  :||...| |...| |...| |...| |...| |...| |...| |...|
650 FAHETQITMQSTVQLRTEYDPHTHVYTTAEPRSEISVQPVTVTQDTLSC 699

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Fig.2A

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Genomic



GlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThr
 GGCCTTAGgtgggggcatcctccctgccccagagctttgccagagtgact
 -----C-----acaggc--c--a-----t-----

ThrSerMetThrValAlaIleHisProProProLeuProGlyAlaTyIleHis
 acctccatgaccgtggccatccaccacccccctgcctggcctacatccat
 -----t-----c-----a--t-----a--a--g---c

ProAlaProAspGluProProTrpSerProAlaAlaThrSerSerGlyGlnLeu
 ccagccctgatgagcccccttggtccctgctgccactagctctggcaacctc
 -----t-c--g-----a-a-a-*

SerSerArgGlyProGlyProAlaThrGly * gProAsnAsnIle *
 agttccaggggaccaggtccagccactgggtga.....agCCCCGAGGAGATCTAG

Parotid gland
Colon

Fetal brain

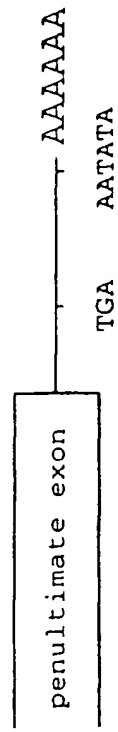


Fig.2B

REPLACEMENT SHEET

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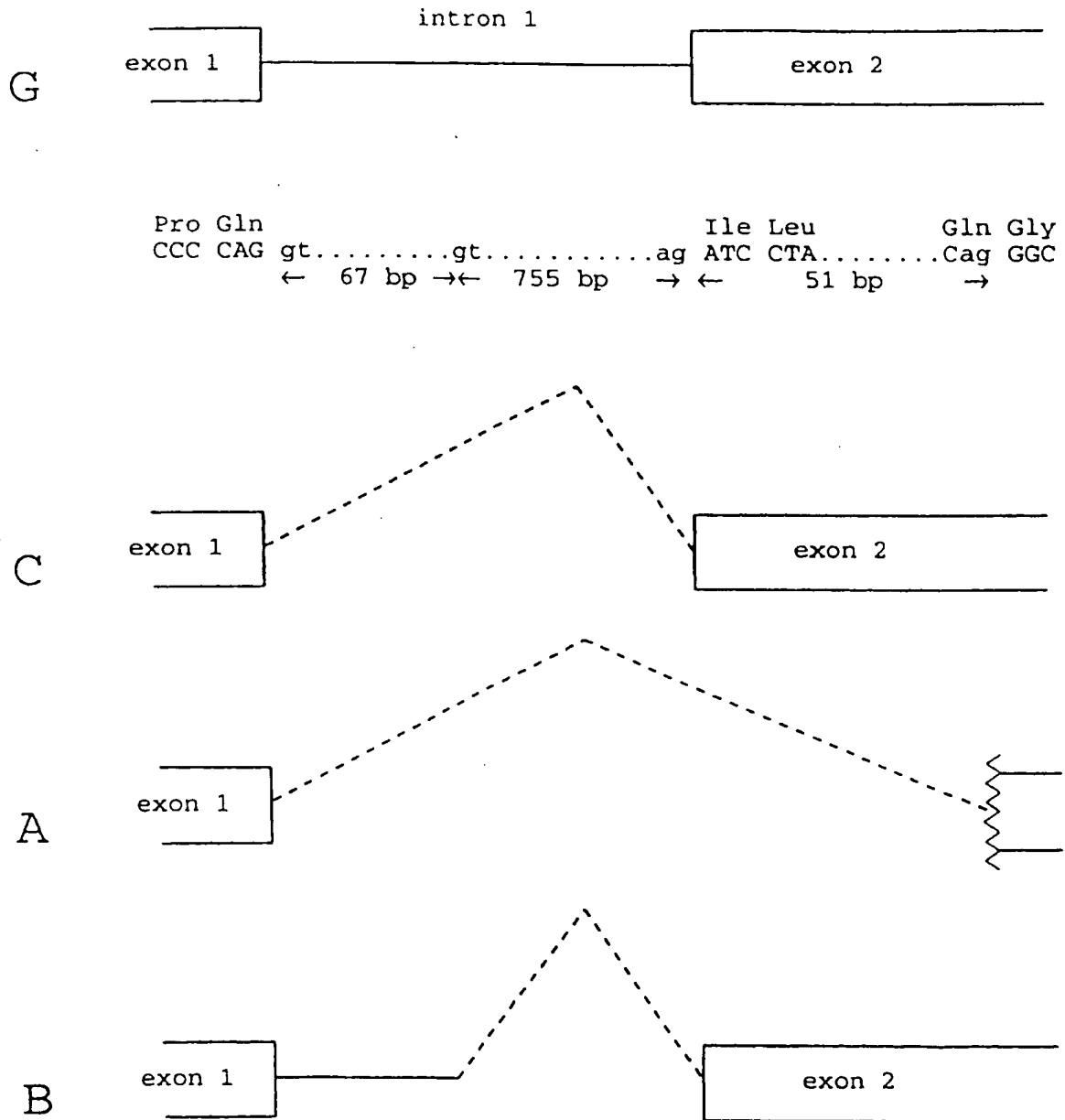


Fig.2C

REPLACEMENT SHEET

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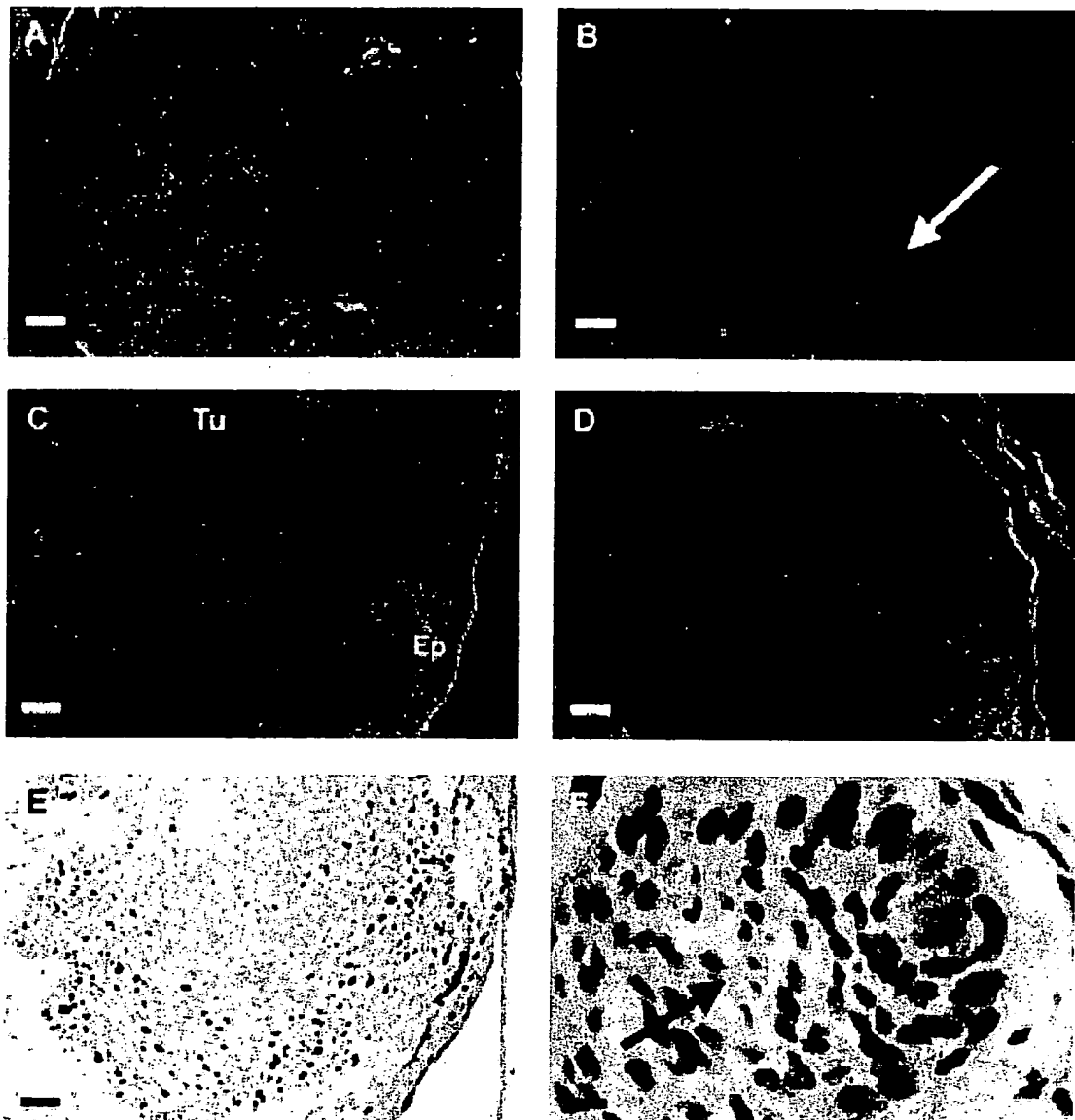


Fig.3

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